Abstract

The invention provides methods, kits and materials for determinining simultaneously signature sequences of a population of tagged polynucleotides. Size ladders of polynucleotide fragments are generated from the population of tagged polynucleotides that contain a plurality of size classes. After the size classes are separated, tags of the separated fragment are copied and labeled according to the identity of one or more bases at the ends of the fragments. In a preferred embodiment, the labeled tags are then specifically hybridized to plurality of identical microarrays of tag complements such that the tags from different size classes are hybridized to separate microarrays. Signature sequences are determined by signals generated at hybridization sites having the same address on each of the plurality of microarrays.